

10/549317

SEQUENCE LISTING

<110> JURIDICAL FOUNDATION THE CHEMO-SERO-THERAPEUTIC RESEARCH INSTITUTE

<120> Composition comprising peptide fragment(s) recognized by antibody against von Willebrand Factor cleaving protease

<130> PH-2095PCT

<140>

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<150> PCT/JP2004/003602

<151> 2004-03-17

<150> JP 2003/71979

<151> 2003-03-17

<160> 18

<210> 1

<211> 1427

<212> PRT

<213> Homo sapiens

<400> 1

Met His Gln Arg His Pro Arg Ala Arg Cys Pro Pro Leu Cys Val

1

5

10

15

Ala Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro

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Ser His Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala		
35	40	45
Val Ser Ser Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro		
50	55	60
Pro Ser Pro Gly Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala		
65	70	75
Ala Gly Gly Ile Leu His Leu Glu Leu Leu Val Ala Val Gly Pro		
80	85	90
Asp Val Phe Gln Ala His Gln Glu Asp Thr Glu Arg Tyr Val Leu		
95	100	105
Thr Asn Leu Asn Ile Gly Ala Glu Leu Leu Arg Asp Pro Ser Leu		
110	115	120
Gly Ala Gln Phe Arg Val His Leu Val Lys Met Val Ile Leu Thr		
125	130	135
Glu Pro Glu Gly Ala Pro Asn Ile Thr Ala Asn Leu Thr Ser Ser		
140	145	150
Leu Leu Ser Val Cys Gly Trp Ser Gln Thr Ile Asn Pro Glu Asp		
155	160	165
Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu Tyr Ile Thr Arg		
170	175	180
Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val Arg Gly Val		
185	190	195
Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys Leu Ile		
200	205	210
Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His Glu		
215	220	225
Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser		

230	235	240
Gly Cys Gly Pro Ser Gly His Val Met	Ala Ser Asp Gly Ala Ala	
245	250	255
Pro Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu		
260	265	270
Leu Ser Leu Leu Ser Ala Gly Arg Ala Arg Cys Val Trp Asp Pro		
275	280	285
Pro Arg Pro Gln Pro Gly Ser Ala Gly His Pro Pro Asp Ala Gln		
290	295	300
Pro Gly Leu Tyr Tyr Ser Ala Asn Glu Gln Cys Arg Val Ala Phe		
305	310	315
Gly Pro Lys Ala Val Ala Cys Thr Phe Ala Arg Glu His Leu Asp		
320	325	330
Met Cys Gln Ala Leu Ser Cys His Thr Asp Pro Leu Asp Gln Ser		
335	340	345
Ser Cys Ser Arg Leu Leu Val Pro Leu Leu Asp Gly Thr Glu Cys		
350	355	360
Gly Val Glu Lys Trp Cys Ser Lys Gly Arg Cys Arg Ser Leu Val		
365	370	375
Glu Leu Thr Pro Ile Ala Ala Val His Gly Arg Trp Ser Ser Trp		
380	385	390
Gly Pro Arg Ser Pro Cys Ser Arg Ser Cys Gly Gly Gly Val Val		
395	400	405
Thr Arg Arg Arg Gln Cys Asn Asn Pro Arg Pro Ala Phe Gly Gly		
410	415	420
Arg Ala Cys Val Gly Ala Asp Leu Gln Ala Glu Met Cys Asn Thr		
425	430	435
Gln Ala Cys Glu Lys Thr Gln Leu Glu Phe Met Ser Gln Gln Cys		

440	445	450
Ala Arg Thr Asp Gly Gln Pro Leu Arg Ser Ser Pro Gly Gly Ala		
455	460	465
Ser Phe Tyr His Trp Gly Ala Ala Val Pro His Ser Gln Gly Asp		
470	475	480
Ala Leu Cys Arg His Met Cys Arg Ala Ile Gly Glu Ser Phe Ile		
485	490	495
Met Lys Arg Gly Asp Ser Phe Leu Asp Gly Thr Arg Cys Met Pro		
500	505	510
Ser Gly Pro Arg Glu Asp Gly Thr Leu Ser Leu Cys Val Ser Gly		
515	520	525
Ser Cys Arg Thr Phe Gly Cys Asp Gly Arg Met Asp Ser Gln Gln		
530	535	540
Val Trp Asp Arg Cys Gln Val Cys Gly Gly Asp Asn Ser Thr Cys		
545	550	555
Ser Pro Arg Lys Gly Ser Phe Thr Ala Gly Arg Ala Arg Glu Tyr		
560	565	570
Val Thr Phe Leu Thr Val Thr Pro Asn Leu Thr Ser Val Tyr Ile		
575	580	585
Ala Asn His Arg Pro Leu Phe Thr His Leu Ala Val Arg Ile Gly		
590	595	600
Gly Arg Tyr Val Val Ala Gly Lys Met Ser Ile Ser Pro Asn Thr		
605	610	615
Thr Tyr Pro Ser Leu Leu Glu Asp Gly Arg Val Glu Tyr Arg Val		
620	625	630
Ala Leu Thr Glu Asp Arg Leu Pro Arg Leu Glu Glu Ile Arg Ile		
635	640	645
Trp Gly Pro Leu Gln Glu Asp Ala Asp Ile Gln Val Tyr Arg Arg		

650	655	660
Tyr Gly Glu Glu Tyr Gly Asn Leu Thr Arg Pro Asp Ile Thr Phe		
665	670	675
Thr Tyr Phe Gln Pro Lys Pro Arg Gln Ala Trp Val Trp Ala Ala		
680	685	690
Val Arg Gly Pro Cys Ser Val Ser Cys Gly Ala Gly Leu Arg Trp		
695	700	705
Val Asn Tyr Ser Cys Leu Asp Gln Ala Arg Lys Glu Leu Val Glu		
710	715	720
Thr Val Gln Cys Gln Gly Ser Gln Gln Pro Pro Ala Trp Pro Glu		
725	730	735
Ala Cys Val Leu Glu Pro Cys Pro Pro Tyr Trp Ala Val Gly Asp		
740	745	750
Phe Gly Pro Cys Ser Ala Ser Cys Gly Gly Gly Leu Arg Glu Arg		
755	760	765
Pro Val Arg Cys Val Glu Ala Gln Gly Ser Leu Leu Lys Thr Leu		
770	775	780
Pro Pro Ala Arg Cys Arg Ala Gly Ala Gln Gln Pro Ala Val Ala		
785	790	795
Leu Glu Thr Cys Asn Pro Gln Pro Cys Pro Ala Arg Trp Glu Val		
800	805	810
Ser Glu Pro Ser Ser Cys Thr Ser Ala Gly Gly Ala Gly Leu Ala		
815	820	825
Leu Glu Asn Glu Thr Cys Val Pro Gly Ala Asp Gly Leu Glu Ala		
830	835	840
Pro Val Thr Glu Gly Pro Gly Ser Val Asp Glu Lys Leu Pro Ala		
845	850	855
Pro Glu Pro Cys Val Gly Met Ser Cys Pro Pro Gly Trp Gly His		

860	865	870
Leu Asp Ala Thr Ser Ala Gly Glu Lys Ala Pro Ser Pro Trp Gly		
875	880	885
Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val Trp Thr Pro Ala		
890	895	900
Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly Leu Met Glu Leu		
905	910	915
Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro Val Gln Glu		
920	925	930
Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg Glu Val		
935	940	945
Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu Ala		
950	955	960
Ala Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu		
965	970	975
Tyr Cys Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu		
980	985	990
Leu Asp Thr Gln Cys Gln Gly Leu Pro Arg Pro Glu Pro Gln Glu		
995	1000	1005
Ala Cys Ser Leu Glu Pro Cys Pro Pro Arg Trp Lys Val Met Ser		
1010	1015	1020
Leu Gly Pro Cys Ser Ala Ser Cys Gly Leu Gly Thr Ala Arg Arg		
1025	1030	1035
Ser Val Ala Cys Val Gln Leu Asp Gln Gly Gln Asp Val Glu Val		
1040	1045	1050
Asp Glu Ala Ala Cys Ala Ala Leu Val Arg Pro Glu Ala Ser Val		
1055	1060	1065
Pro Cys Leu Ile Ala Asp Cys Thr Tyr Arg Trp His Val Gly Thr		

1070	1075	1080
Trp Met Glu Cys Ser Val Ser Cys Gly Asp Gly Ile Gln Arg Arg		
1085	1090	1095
Arg Asp Thr Cys Leu Gly Pro Gln Ala Gln Ala Pro Val Pro Ala		
1100	1105	1110
Asp Phe Cys Gln His Leu Pro Lys Pro Val Thr Val Arg Gly Cys		
1115	1120	1125
Trp Ala Gly Pro Cys Val Gly Gln Gly Thr Pro Ser Leu Val Pro		
1130	1135	1140
His Glu Glu Ala Ala Ala Pro Gly Arg Thr Thr Ala Thr Pro Ala		
1145	1150	1155
Gly Ala Ser Leu Glu Trp Ser Gln Ala Arg Gly Leu Leu Phe Ser		
1160	1165	1170
Pro Ala Pro Gln Pro Arg Arg Leu Leu Pro Gly Pro Gln Glu Asn		
1175	1180	1185
Ser Val Gln Ser Ser Ala Cys Gly Arg Gln His Leu Glu Pro Thr		
1190	1195	1200
Gly Thr Ile Asp Met Arg Gly Pro Gly Gln Ala Asp Cys Ala Val		
1205	1210	1215
Ala Ile Gly Arg Pro Leu Gly Glu Val Val Thr Leu Arg Val Leu		
1220	1225	1230
Glu Ser Ser Leu Asn Cys Ser Ala Gly Asp Met Leu Leu Leu Trp		
1235	1240	1245
Gly Arg Leu Thr Trp Arg Lys Met Cys Arg Lys Leu Leu Asp Met		
1250	1255	1260
Thr Phe Ser Ser Lys Thr Asn Thr Leu Val Val Arg Gln Arg Cys		
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Gly Arg Pro Gly Gly Gly Val Leu Leu Arg Tyr Gly Ser Gln Leu		

1280	1285	1290
Ala Pro Glu Thr Phe Tyr Arg Glu Cys Asp Met Gln Leu Phe Gly		
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Pro Trp Gly Glu Ile Val Ser Pro Ser Leu Ser Pro Ala Thr Ser		
1310	1315	1320
Asn Ala Gly Gly Cys Arg Leu Phe Ile Asn Val Ala Pro His Ala		
1325	1330	1335
Arg Ile Ala Ile His Ala Leu Ala Thr Asn Met Gly Ala Gly Thr		
1340	1345	1350
Glu Gly Ala Asn Ala Ser Tyr Ile Leu Ile Arg Asp Thr His Ser		
1355	1360	1365
Leu Arg Thr Thr Ala Phe His Gly Gln Gln Val Leu Tyr Trp Glu		
1370	1375	1380
Ser Glu Ser Ser Gln Ala Glu Met Glu Phe Ser Glu Gly Phe Leu		
1385	1390	1395
Lys Ala Gln Ala Ser Leu Arg Gly Gln Tyr Trp Thr Leu Gln Ser		
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Trp Val Pro Glu Met Gln Asp Pro Gln Ser Trp Lys Gly Lys Glu		
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Gly Thr		
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<213>Homo sapiens

<400>4

ccaacctgac cagtgtctac attgccaacc 30

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<211>21

<212>DNA

<213>Homo sapiens

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ctggagccct gccacctag g 21

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<212>DNA

<213>Homo sapiens

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cg

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<212>DNA

<213>Homo sapiens

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at 62

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<213>Homo sapiens

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tg 62

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<210>14

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62

<210>15

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60

cc

62

<210>16

<211>60

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<213>Homo sapiens

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<211>27

<212>DNA

<213>Artificial Sequence

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<223>Description of Artificial Sequence:Synthetic DNA

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gactacaagg acgatgacga taagtga

27

<210>18

<211>8

<212>RPT

<213>Artificial Sequence

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<223>Description of Artificial Sequence:Synthetic peptide

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Asp Tyr Lys Asp Asp Asp Asp Lys

1

5